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OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 16:36:47 ; Search time 0.001 Seconds  
(without alignments)

34.620 Million cell updates/sec

Title: us-09-954-556-3

Perfect score: 30

Sequence: 1 cacgaccaagaaggcagactttagcggcc 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 44 seqs, 577 residues

Total number of hits satisfying chosen parameters: 88

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 44 summaries

Database : rni.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match	Length	DB	ID	Description
1	14.4	48.0	17	1	US-08-541-950B-17	Sequence 17, Appl
2	14.4	48.0	17	1	US-08-541-950B-20	Sequence 20, Appl
3	14.4	48.0	17	1	US-09-083-756A-17	Sequence 17, Appl
4	14.4	48.0	17	1	US-09-083-756A-20	Sequence 20, Appl
5	14.4	48.0	18	1	US-08-541-950B-23	Sequence 23, Appl
6	14.4	48.0	18	1	US-09-083-756A-23	Sequence 23, Appl
7	13.8	46.0	17	1	US-09-325-601-1	Sequence 1, Appl
8	13.8	46.0	18	1	US-08-541-950B-13	Sequence 13, Appl
9	13.8	46.0	18	1	US-09-083-756A-13	Sequence 13, Appl
10	13.8	46.0	18	1	US-09-325-601-3	Sequence 3, Appl
11	12.8	42.7	17	1	US-08-541-950B-18	Sequence 18, Appl
12	12.8	42.7	17	1	US-08-541-950B-19	Sequence 19, Appl
13	12.8	42.7	17	1	US-08-541-950B-21	Sequence 21, Appl
14	12.8	42.7	17	1	US-08-541-950B-22	Sequence 22, Appl
15	12.8	42.7	17	1	US-09-083-756A-18	Sequence 18, Appl
16	12.8	42.7	17	1	US-09-083-756A-19	Sequence 19, Appl
17	12.8	42.7	17	1	US-09-083-756A-21	Sequence 21, Appl
18	12.8	42.7	17	1	US-09-083-756A-22	Sequence 22, Appl
19	11.8	39.3	15	1	US-08-363-240A-47	Sequence 47, Appl
20	11.4	38.0	15	1	US-08-073-65	Sequence 65, Appl
21	9.4	31.3	12	1	US-09-281-418-65	Sequence 25, Appl
22	9	30.0	10	1	US-09-508-753B-25	Sequence 36, Appl
23	8.4	28.0	10	1	US-09-263-790-36	Sequence 18, Appl
24	8.4	28.0	10	1	US-09-721-777-18	Sequence 20, Appl
25	8.4	28.0	10	1	US-08-545-253A-20	Sequence 20, Appl
26	8.4	28.0	10	1	US-08-719-337-20	Sequence 20, Appl
27	8.4	28.0	10	1	US-09-255-432-6	Sequence 6, Appl
28	8.4	28.0	10	1	US-08-878-835A-12	Sequence 12, Appl
29	8.4	28.0	10	1	US-09-508-753B-28	Sequence 13, Appl
30	8.4	28.0	10	1	US-09-508-753B-63	Sequence 11, Appl
31	8.4	28.0	10	1	US-08-894-454-10	Sequence 6, Appl
32	8.4	28.0	10	1	US-09-518-454-16	Sequence 342, Appl
33	8.4	28.0	11	1	US-08-173-489C-342	Sequence 20, Appl

**ALIGNMENTS**

RESULT 1  
US-08-541-950B-17  
Sequence 17, Application US/08541950B  
Patent No. 5821046

GENERAL INFORMATION:

APPLICANT: Karr J, Gait MJ, Heaphy S, Dingwall C

TITLE OF INVENTION: VIRAL (HIV) GROWTH INHIBITION

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.

STREET: One Financial Center, 45th Floor

CITY: Boston

STATE: MA

ZIP: 02111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/541-950B

FILING DATE: 10/10/95

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/960, 370

FILING DATE: 03/10/93

ATTORNEY/AGENT INFORMATION:

NAME: Williams, Ph.D., Kathleen M.

REGISTRATION NUMBER: 34, 380

REFERENCE DOCKET NUMBER: 3777/57347 (MRC-011X)

TELECOMMUNICATION INFORMATION:

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INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic RNA

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 8

OTHER INFORMATION: N is 2'-deoxythymidine

Query US-08-541-950B-17

US-08-541-950B-17

Query Match 48.0% ; Score 14.4; DB 1; Length 17;  
Best Local Similarity 76.5%; Ped. No. 2, 9;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 AGCCAGAGCTCGCAGC 1506

Sequence 1490 AGCCAGAGCTCGCAGC 1506

Sequence 342, Appl

Sequence 20, Application US/08541950B

Sequence 20, Application US/08541950B



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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 15, 2004, 16:35:35 ; Search time 0.001 seconds  
(without alignments)

98.460 Million cell updates/sec

Title: us-09-954-556-3

Perfect score: 30

Sequence: 1 cacgaccagaaggccagacttcagcagcca 30

Scoring table: IDENTITY\_NUC

GAPOP\_10.0 , Gapext 0.5

Searched: 143 seqs, 1641 residues

Total number of hits satisfying chosen parameters: 286

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 143 summaries

Database : rng.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	%	Match Length	DB ID	Description
1	13.8	46.0	17	1	AAQ24060	Artificial HIV-1 T
2	13.8	46.0	17	1	AAZ19070	HIV-1 TAR oligonuc
3	13.8	46.0	17	1	ABK6439	Waxy starch produc
4	13.8	46.0	17	1	ABK6440	Waxy starch produc
5	13.8	46.0	18	1	AAZ19072	HIV-1 TAR oligonuc
6	13.8	46.0	18	1	AAFP4454	Human PR02 gene-sp
7	13.8	46.0	18	1	AAFT4457	Human PR02 gene-sp
8	12.4	41.3	15	1	AAK7556	Antisense oligo #5
9	12.4	41.3	15	1	AAFP9086	IGF-I oligonucleot
10	12.4	41.3	15	1	AAFP9087	IGF-I oligonucleot
11	12	40.0	14	1	AAZ24832	Substrate for hair
12	12	40.0	14	1	AAFP1669	Hepatitis C virus
13	12	40.0	15	1	AAFP9084	IGF-I oligonucleot
14	12	40.0	15	1	AAFP9085	IGF-I oligonucleot
15	11.8	39.3	15	1	AAFP9619	Human CTPP HH ribo
16	11.8	39.3	15	1	AAFP7839	IGFBP3 oligonucleo
17	11.4	38.0	15	1	AAZ15764	Antisense oligo #3
18	11.4	38.0	15	1	AAZ25973	Histoplasma capsu
19	11.4	38.0	15	1	AAFP9088	IGF-I oligonucleot
20	10.8	36.0	14	1	AAZ24816	Substrate for hair
21	10.8	36.0	14	1	AAFP9958	Geminivirus Rep re
22	10.8	36.0	14	1	ABX01653	Hepatitis C virus
23	10.4	34.7	13	1	ABFP8234	Oligonucleotide SB
24	10.4	34.7	13	1	ABFP8235	Oligonucleotide SB
25	10.4	33.3	10	1	AAZ78899	Human dendritic ce
26	10	33.3	10	1	AAZ3653	Metastatic breast
27	10	33.3	10	1	AAFP9527	Yeast NORF gene SA
28	10	33.3	10	1	AAFP4162	Yeast NORF gene SA
29	10	33.3	10	1	AAFP9463	Yeast NORF gene SA
30	10	33.3	10	1	AAFP1899	Yeast NORF gene SA
31	10	33.3	12	1	AAV2260	Random Primed lne
32	10	33.3	13	1	AAKP9228	PCR primer R-AP34
33	10	33.3	13	1	ADCP4953	Camellia sinensis

Run on: April 15, 2004, 16:33:22 ; Search time 0.001 seconds  
 (without alignments)  
 79,200 Million cell updates/sec

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OM nucleic - nucleic search, using sw model

GenCore version 5.1.6

Title: us-09-954-556-3  
 Perfect score: 30  
 Sequence: 1 caccgaccaagaaggccagacttacgcagcca 30

Scoring table: IDENTITY.NUC  
 GapP 10.0 , GapExt 0.5

Searched: 102 seqs, 1320 residues

Total number of hits satisfying chosen parameters: 204

Minimum DB seq length: 8  
 Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 102 summaries

Database : rge.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query	Length	DB	ID	Description
1	14.4	48.0	17	1	AR048076	ACCESSION AR048076
2	14.4	48.0	17	1	AR048079	ACCESSION AR048079
3	14.4	48.0	17	1	AR108979	ACCESSION AR108979
4	14.4	48.0	17	1	AR108932	ACCESSION AR108932
5	14.4	48.0	18	1	AR048082	ACCESSION AR048082
6	14.4	48.0	18	1	AR108985	ACCESSION AR108985
7	13.8	46.0	17	1	A20708	ACCESSION A20708
8	13.8	46.0	17	1	A21027	ACCESSION A21027
9	13.8	46.0	17	1	AR249433	ACCESSION AR249433
10	13.8	46.0	17	1	AR340497	ACCESSION AR340497
11	13.8	46.0	17	1	AX008727	ACCESSION AX008727
12	13.8	46.0	17	1	AX325651	ACCESSION AX325651
13	13.8	46.0	17	1	AX325652	ACCESSION AX325652
14	13.8	46.0	18	1	A21030	ACCESSION A21030
15	13.8	46.0	18	1	AR048072	ACCESSION AR048072
16	13.8	46.0	18	1	AR108975	ACCESSION AR108975
17	13.8	46.0	18	1	BD249435	ACCESSION BD249435
18	13.8	46.0	18	1	BD340499	ACCESSION BD340499
19	13.8	46.0	18	1	AX008729	ACCESSION AX008729
20	13.8	46.0	18	1	AX084246	ACCESSION AX084246
21	13.8	46.0	18	1	AX084249	ACCESSION AX084249
22	12.8	42.7	17	1	AR048077	ACCESSION AR048077
23	12.8	42.7	17	1	AR048078	ACCESSION AR048078
24	12.8	42.7	17	1	AR048080	ACCESSION AR048080
25	12.8	42.7	17	1	AR048081	ACCESSION AR048081
26	12.8	42.7	17	1	AR108980	ACCESSION AR108980
27	12.8	42.7	17	1	AR108981	ACCESSION AR108981
28	12.8	42.7	17	1	AR108983	ACCESSION AR108983
29	12.8	42.7	17	1	AR108984	ACCESSION AR108984
30	12.0	40.0	14	1	BD209410	ACCESSION BD209410
31	12.0	40.0	15	1	A12791	ACCESSION A12791
32	11.4	38.0	15	1	A127893	ACCESSION A127893
33	36.7	14	1		AR39566	ACCESSION AR39566

## ALIGNMENTS